

10/551655

8062-1031

SEQUENCE LISTING

JC20 Rec'd PCT/PTO 28 SEP 2009

<110> Nihon university

<120> POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE DEHYDRATASE AND USE THEREOF

<130> 10465

<150> JP 2003-092337

<151> 2003-3-28

<160> 10

<210> 1

<211> 328

<212> PRT

<213> Glycyrrhiza echinata

<220>

<223> Inventor: Ayabe, Shin-ichi

Inventor: Aoki, Toshio

Inventor: Akashi, Tomoyoshi

<400> 1

Met Ala Ser Ser Thr Ser Thr Thr Ser Lys Glu Ile Asp Arg Glu

1

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15

Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp Gly Thr Val Glu Arg Phe

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25

30

Leu Gly Ser Ser Phe Val Pro Pro Ser Pro Glu Asp Pro Glu Thr Gly

35	40	45
Val Ser Thr Lys Asp Ile Val Ile Ser Glu Asn Pro Thr Ile Ser Ala		
50	55	60
Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr Thr Glu Lys Leu Pro Ile		
65	70	75
Leu Val Tyr Tyr His Gly Gly Ala Phe Cys Leu Glu Ser Ala Phe Ser		
85	90	95
Phe Leu His Gln Arg Tyr Leu Asn Ile Val Ala Ser Lys Ala Asn Val		
100	105	110
Leu Val Val Ser Ile Glu Tyr Arg Leu Ala Pro Glu His Pro Leu Pro		
115	120	125
Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu Lys Trp Val Thr Ser His		
130	135	140
Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala Asp Pro Trp Leu Ile Lys		
145	150	155
His Gly Asp Phe Asn Arg Phe Tyr Ile Gly Gly Asp Thr Ser Gly Ala		
165	170	175
Asn Ile Ala His Asn Ala Ala Leu Arg Val Gly Ala Glu Ala Leu Pro		
180	185	190

Gly Gly Leu Arg Ile Ala Gly Val Leu Ser Ala Phe Pro Leu Phe Trp
195 200 205

Gly Ser Lys Pro Val Leu Ser Glu Pro Val Glu Gly His Glu Lys Ser
210 215 220

Ser Pro Met Gln Val Trp Asn Phe Val Tyr Pro Asp Ala Pro Gly Gly
225 230 235 240

Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala Pro Gly Ala Pro Asn Leu
245 250 255

Ala Thr Leu Gly Cys Pro Lys Met Leu Val Phe Val Ala Gly Lys Asp
260 265 270

Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr Glu Ala Val Lys Glu Ser
275 280 285

Gly Trp Lys Gly Asp Val Glu Leu Ala Gln Tyr Glu Gly Glu Glu His
290 295 300

Cys Phe Gln Ile Tyr His Pro Glu Thr Glu Asn Ser Lys Asp Leu Ile
305 310 315 320

Gly Arg Ile Ala Ser Phe Leu Val

<210> 2

<211> 1178

<212> DNA

<213> Glycyrrhiza echinata

<400> 2

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aaa gag ata gac agg gag ctt cct cct ctt ctc cgg gtc tac aaa gat	100
Lys Glu Ile Asp Arg Glu Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp	
15 20 25	
gga acc gtg gag cga ttc cta ggc tca tcg ttt gta cca cct tcc cct	148
Gly Thr Val Glu Arg Phe Leu Gly Ser Ser Phe Val Pro Pro Ser Pro	
30 35 40	
gaa gac ccc gaa aca ggg gtt tcc acg aaa gac ata gta atc tca gaa	196
Glu Asp Pro Glu Thr Gly Val Ser Thr Lys Asp Ile Val Ile Ser Glu	
45 50 55	
aac ccc acc atc tct gct cgc gtt tac ctt cca aaa ctg aac aac acc	244
Asn Pro Thr Ile Ser Ala Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr	
60 65 70	
acc gag aag ctc cca atc ttg gtc tac tac cac ggc ggc gcg ttc tgc	292
Thr Glu Lys Leu Pro Ile Leu Val Tyr Tyr His Gly Gly Ala Phe Cys	
75 80 85 90	
ctc gaa tct gct ttc tcc ttc ctc cac caa cgc tac ctc aac atc gtt	340

Leu Glu Ser Ala Phe Ser Phe Leu His Gln Arg Tyr Leu Asn Ile Val	
95 100 105	
gct tcc aag gca aat gtt cta gta gtt tcc atc gag tac agg ctc gcc	388
Ala Ser Lys Ala Asn Val Leu Val Val Ser Ile Glu Tyr Arg Leu Ala	
110 115 120	
cca gaa cac cct ctt ccg gct gca tat gaa gat ggt tgg tat gct ctc	436
Pro Glu His Pro Leu Pro Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu	
125 130 135	
aaa tgg gtc act tct cat tcc aca aac aac aac aaa ccc acc aac gct	484
Lys Trp Val Thr Ser His Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala	
140 145 150	
gac cca tgg ttg atc aaa cac ggt gat ttc aac agg ttc tac atc ggg	532
Asp Pro Trp Leu Ile Lys His Gly Asp Phe Asn Arg Phe Tyr Ile Gly	
155 160 165 170	
ggt gac act tct ggt gca aac att gca cac aat gcg gct ctt cgt gtt	580
Gly Asp Thr Ser Gly Ala Asn Ile Ala His Asn Ala Ala Leu Arg Val	
175 180 185	
ggt gct gag gcc tta cct ggg ggg ctg aga ata gca ggg gta ctc tct	628
Gly Ala Glu Ala Leu Pro Gly Gly Leu Arg Ile Ala Gly Val Leu Ser	
190 195 200	
gct ttt cct ctg ttt tgg ggt tct aag cct gtt ttg tca gaa cct gtc	676
Ala Phe Pro Leu Phe Trp Gly Ser Lys Pro Val Leu Ser Glu Pro Val	

205	210	215	
gag ggg cat gag aag agc tca ccc atg caa gtt tgg aac ttt gtg tac			724
Glu Gly His Glu Lys Ser Ser Pro Met Gln Val Trp Asn Phe Val Tyr			
220	225	230	
cca gat gca cca ggt ggc ata gat aac cca cta atc aac cct ttg gca			772
Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala			
235	240	245	250
cct ggg gct cct aac ttg gcc aca ctt ggg tgt cca aag atg ttg gtc			820
Pro Gly Ala Pro Asn Leu Ala Thr Leu Gly Cys Pro Lys Met Leu Val			
	255	260	265
ttt gtt gcg ggg aag gat gat ctt aga gac aga ggg att tgg tac tat			868
Phe Val Ala Gly Lys Asp Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr			
	270	275	280
gag gct gtg aag gaa agt ggg tgg aaa ggg gat gtg gaa ctt gct cag			916
Glu Ala Val Lys Glu Ser Gly Trp Lys Gly Asp Val Glu Leu Ala Gln			
	285	290	295
tat gaa ggg gag gaa cat tgc ttc cag atc tac cat cct gaa act gag			964
Tyr Glu Gly Glu Glu His Cys Phe Gln Ile Tyr His Pro Glu Thr Glu			
	300	305	310
aat tct aaa gat ctc atc ggt cgc atc gct tcc ttc ctt gtt tga acaca			1014
Asn Ser Lys Asp Leu Ile Gly Arg Ile Ala Ser Phe Leu Val			
	315	320	325

cagctagact tcgggttcat tattactagt atgtgatttt gtttgattaa tgttttgtca 1074
tcaattgatg ggtaataaat tggattaggg tactagggtt cctgaatcat gctcaatttt 1134
acttttcctg tactattact tgtttatgaa agaattaatg gcat 1178

<210> 3

<211> 319

<212> PRT

<213> Glycine max

<400> 3

Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr

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Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala

20 25 30

Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile

35 40 45

Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His

50 55 60

His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala

65 70 75 80

Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn

	85	90	95
Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg			
	100	105	110
Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr			
	115	120	125
Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn			
	130	135	140
Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val			
	145	150	155
			160
Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg			
	165	170	175
Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu			
	180	185	190
Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala			
	195	200	205
Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala			
	210	215	220
Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys			
	225	230	235
			240

Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu

245

250

255

Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr

260

265

270

His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe

275

280

285

Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr

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295

300

His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val

305

310

315

<210> 4

<211> 19

<212> 960

<213> Glycine max

<223> DNA

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Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr

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15

aag gat ggc agc gtg gag cgt ctt cta agc tct gaa aac gtg gca gcc	96
Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala	
20 25 30	
tcc cct gaa gat ccc caa act gga gtc tca tcc aaa gac ata gtc atc	144
Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile	
35 40 45	
gca gac aac ccc tac gtc tcc gct cgc att ttc ctt ccc aaa tcc cac	192
Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His	
50 55 60	
cac act aac aac aaa ctc ccc atc ttc ctc tac ttc cac ggt ggc gcc	240
His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala	
65 70 75 80	
ttt tgc gtc gaa tcc gcc ttc tcc ttt ttc gtc cac cgc tat ctc aac	288
Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn	
85 90 95	
atc ttg gcc tca gaa gcc aac ata ata gcc atc tcc gtc gac ttc aga	336
Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg	
100 105 110	
ctc ctc cca cac cac cct atc cct gct gcc tac gaa gac ggt tgg acc	384
Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr	
115 120 125	
acc ctc aaa tgg att gct tcc cac gcc aac aac acc aac acc acc aac	432

Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn

130

135

140

ccg gag cca tgg cta ctc aac cac gcc gac ttc acc aaa gtc tac gta 480

Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val

145

150

155

160

gga ggt gaa acc agc ggt gct aac atc gca cac aac ctg ctt ttg cgt 528

Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg

165

170

175

gca ggt aac gaa tcc ctc ccc ggg gat ctg aaa ata ttg ggt gga tta 576

Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu

180

185

190

cta tgc tgc ccc ttc ttc tgg ggc tcg aag cca att ggg tcg gag gct 624

Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala

195

200

205

gtt gag ggg cac gag cag agt ttg gcc atg aag gtc tgg aac ttt gcc 672

Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala

210

215

220

tgc cct gat gcc ccc ggt gga atc gat aac ccc tgg atc aac ccc tgt 720

Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys

225

230

235

240

gtt cct ggg gca ccc tct ttg gcc act ctt gcc tgc tct aag ttg ctc 768

Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu

245	250	255	
gtt act atc act ggc aaa gac gag ttc aga gac aga gat att ctc tac			816
Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr			
260	265	270	
cac cac acc gtt gag caa agt ggc tgg caa ggt gaa ctt caa ctc ttt			864
His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe			
275	280	285	
gat gct ggc gat gag gag cat gct ttc cag ctc ttc aag cct gag act			912
Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr			
290	295	300	
cat ctt gct aaa gcc atg atc aaa cgc ttg gct tct ttt ctg gtt tga			960
His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val			
305	310	315	

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<400> 5

gtcatatggc gaaggagata gtgaa 25

<210> 6

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 6

agggatccat caaaccagaa aaga 24

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<400> 7

gtcatatggc ttcttcaacc tcaac 25

<210> 8

<211> 25

<212> DNA

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<400> 8

ctggatcctc aaacaaggaa ggaag 25

<210> 9

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<212> DNA

<213> Artificial Sequence

<400> 9

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<210> 10

<211> 30

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<400> 10

gggagctcga gtcaaaccag aaaagaagcc 30